

WHAT IS CLAIMED IS:

1. A method of obtaining plants characterized by enhanced growth and/or commercial yield under growth limiting conditions, the method comprising:
 - (a) obtaining a population of plants transformed to express a polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13;
 - (b) growing said population of plants under the growth limiting condition to thereby detect plants of said population having enhanced growth and/or commercial yield; and
 - (c) selecting plants expressing said polypeptide having enhanced growth and/or commercial yield as compared to control plants,thereby obtaining plants characterized by enhanced growth and/or commercial yield under growth limiting conditions.
2. The method of claim 1, wherein said amino acid sequence is as set forth by SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13.
3. The method of claim 1, wherein step (a) is effected by transforming at least a portion of the plants of said population with a nucleic acid construct comprising a polynucleotide region encoding said polypeptide.
4. The method of claim 3, wherein said transforming is effected by a method selected from the group consisting of *Agrobacterium* mediated transformation, viral infection, electroporation and particle bombardment.
5. The method of claim 3, wherein said nucleic acid construct further comprises a second polynucleotide region encoding a transit peptide, said second polynucleotide being operably linked to said polynucleotide region encoding said polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13.

6. The method of claim 3, wherein said nucleic acid construct further comprises a promoter sequence operably linked to said polynucleotide region encoding said polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13.

7. The method of claim 6, wherein said nucleic acid construct further comprises a promoter sequence operably linked to both said polynucleotide region encoding said polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13 and to said second polynucleotide region.

8. The method of claim 6, wherein said promoter is functional in eukaryotic cells.

9. The method of claim 6, wherein said promoter is selected from the group consisting of a constitutive promoter, an inducible promoter, a developmentally regulated promoter and a tissue specific promoter.

10. The method of claim 1, wherein said plants are C3 plants.

11. The method of claim 10, wherein said C3 plants are selected from the group consisting of tomato, soybean, potato, cucumber, cotton, wheat, rice, barley, lettuce, solidago, banana and poplar.

12. The method of claim 1, wherein said plants are C4 plants.

13. The method of claim 12, wherein said C4 plants are selected from the group consisting of corn, sugar cane and sorghum.

14. The method of claim 1, wherein said enhanced growth is a growth rate at least 10 % higher than that of a control plant grown under similar growth conditions.

15. The method of claim 1, wherein said growth limiting condition is selected from the group consisting of water stress, low humidity, salt stress, and low CO₂ conditions.

16. The method of claim 15, wherein said low humidity is humidity lower than 40 %.

17. The method of claim 15, wherein said low CO₂ (limiting conditions) is an intercellular CO₂ concentration lower than 10 micromolar.

18. The method of claim 14, wherein said growth rate is determined by at least one growth parameter selected from the group consisting of increased fresh weight, increased dry weight, increased root growth, increased shoot growth and increased flower development over time.

19. A transformed crop comprising a population of transformed plants expressing a polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13 wherein each individual plant of said population is characterized by enhanced growth under limiting conditions as compared to similar non transformed plants when grown under at least one growth limiting condition.

20. The transformed crop of claim 19, wherein said amino acid sequence is as set forth by SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13.

21. The transformed crop of claim 19, wherein said transformed plants are C3 plants.

22. The transformed crop of claim 21, wherein said C3 plants are selected from the group consisting of tomato, soybean, potato, cucumber, cotton, wheat, rice, barley, lettuce, solidago, banana, poplar and citrus.

23. The transformed crop of claim 19, wherein said transformed plants are C4 plants.

24. The transformed crop of claim 23, wherein said C4 plants are selected from the group consisting of corn, sugar cane and sorghum.

25. The transformed crop of claim 19, wherein a growth rate of said population of transformed plants is at least 10 % higher than that of a population of similar non transformed plants when both are grown under a similar growth limiting condition.

26. The transformed crop of claim 25, wherein said growth rate is determined by at least one growth parameter selected from the group consisting of fresh weight, dry weight, root growth, shoot growth and flower development.

27. The transformed crop of claim 19, wherein said transformed plant is further characterized by an increased commercial yield as compared to similar non transformed plant grown under similar conditions.

28. The transformed crop of claim 19, wherein said at least one growth limiting condition is selected from the group consisting of water stress, low humidity, salt stress, and/or low CO₂ conditions.

29. The transformed crop of claim 28, wherein said low humidity is humidity lower than 40 %.

30. The transformed crop of claim 28, wherein said low CO₂ is an intercellular CO₂ concentration lower than 10 micromolar.

31. A nucleic acid expression construct comprising:
- (a) a first polynucleotide region encoding a polypeptide including an amino acid sequence at least 60 % homologous to that set forth by SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13; and
 - (b) a second polynucleotide region comprising a promoter sequence operably linked to said first polynucleotide region, said promoter sequence being functional in eukaryotic cells.

32. The nucleic acid expression construct of claim 31, wherein said promoter is selected from the group consisting of a constitutive promoter, an inducible promoter, a developmentally regulated promoter and a tissue specific promoter.

33. The nucleic acid expression construct of claim 31, wherein said promoter is a plant promoter.

34. The nucleic acid expression construct of claim 31, further comprising a second polynucleotide region encoding a transit peptide, said second polynucleotide being operably linked to said polynucleotide region encoding said polypeptide having an amino acid sequence at least 60 % homologous to that set forth in SEQ ID NOs: 3, 5, 6, 7, 10, 11, 12 or 13.